WHAT IS CLAIMED IS:

1. A method of identifying a polypeptide comprising a functional domain of interest comprising:

(a) contacting a multivalent recognition unit complex with a plurality of polypeptides; and

(b) identifying a polypeptide having a selective binding affinity for said recognition unit complex.

2. The method of claim 1 in which said plurality of polypeptides is from a polypeptide expression library.

3. The method of claim 1 in which said plurality of polypeptides is obtained from a virus.

4. The method of claim 2 in which said expression library is a cDNA expression library.

5. The method of claim 2 in which said expression library is a genomic DNA library.

6. The method of claim 2 in which said expression library is a recombinant bacteriophage library.

7. The method of claim 6 in which said recombinant bacteriophage library is a recombinant M13 library.

8. The method of claim 2 in which said expression library is a recombinant plasmid or cosmid library.

9. The method of claim 1 in which the recognition unit is a peptide.

10. The method of claim 1 in which said recognition unit is a peptide having less than about 140 amino acid residues.

11. The method of claim 1 in which said recognition unit is a peptide having less than about 100 amino acid residues.

12. The method of claim 1 in which said recognition unit is a peptide having less than about 70 amino acid residues.

13. The method of claim 1 in which said recognition unit is a peptide having about 6 to 60 amino acid residues.

14. The method of claim 1 in which said recognition unit is a peptide having 20 to 50 amino acid residues.

15. The method of claim 1 in which the valency of the recognition unit in the complex is at least two.

16. The method of claim 9 in which the valency of the recognition unit in the complex is at least two.

17. The method of claim 1 in which the valency of the recognition unit in the complex is at least four.

18. The method of claim 9 in which the valency of the recognition unit in the complex is at least four.

19. The method of claim 17 in which the recognition unit complex is a complex comprising (a) avidin or streptavidin, and (b) biotinylated recognition units.

20. The method of claim 18 in which the recognition unit complex is a complex comprising (a) avidin or streptavidin, and (b) the biotinylated peptides.

21. The method of claim 2 in which said identifying step comprises selecting a positive clone, which harbors a DNA construct encoding a polypeptide having a selective affinity for said recognition unit and which polypeptide includes the functional domain of interest or a functional equivalent thereof.

22. The method of claim 21 which further comprises determining the coding sequence of said DNA construct.

23. The method of claim 22 which further comprises deducing an amino acid sequence from said coding sequence.

24. The method of claim 1 in which said contacting step comprises immobilizing said recognition unit complex on a solid support and bringing a solution containing said plurality of polypeptides in contact with said immobilized recognition unit complex.

25. The method of claim 1 in which said contacting step comprises separating said plurality of polypeptides and bringing a solution of said recognition unit complex in contact with said separated polypeptides.

26. The method of claim 1 in which said identifying step includes selecting a polypeptide, among said plurality of polypeptides, having a selective affinity for said recognition unit and determining the amino acid sequence of said polypeptide.

27. The method of claim 1 in which said plurality of polypeptides is immobilized on a solid support.

28. The method of claim 27 in which said contacting step comprises contacting said solid support with a solution containing said recognition unit complex.

29. The method of claim 28 which further comprises washing away any unbound recognition unit complex.

30. The method of claim 29 which further comprises detecting any recognition unit complex that remains bound to said solid support.

31. The method of claim 1 in which said selective binding affinity is on the order of about 1 nM to about 1 mM.

32. The method of claim 1 in which said selective binding affinity is on the order of about 10 nM to about 100 μM.

33. The method of claim 1 in which said selective binding affinity is on the order of about 100 nm to about 10 μM.

34. The method of claim 1 in which said selective binding affinity is on the order of about 100 nm to about 1 μM.

35. The method of claim 9 in which said peptide is chosen from a random peptide library.

36. A method of identifying a polypeptide comprising a functional domain of interest comprising:

(a) contacting a multivalent recognition unit complex, which complex comprises (i) avidin or streptavidin, and (ii) biotinylated recognition units, with a plurality of polypeptides from a cDNA expression library, in which the recognition unit is a peptide having in the range of 6 to 60 amino acid residues; and

(b) identifying a polypeptide having a selective binding affinity for said recognition unit complex.

37. The method of claim 4 or 36 in which the cDNA expression library is a human cDNA expression library.

38. The method of claim 36 in which the peptide is previously identified by a method comprising screening a random peptide library to identify a peptide having selective binding affinity for the functional domain of interest or a functional equivalent thereof.

39. The method of claim 36 in which the functional domain of interest is a domain selected from the group consisting of an SH1, SH2, SH3, PH, PTB, LIM, armadillo, Notch/ankyrin repeat, zinc finger, leucine zippers, and helix-turn-helix.

40. The method of claim 1 in which the functional domain of interest is a domain selected from the group consisting of an SH1, SH2, SH3, PH, PTB, LIM, armadillo, Notch/ankyrin repeat, zinc finger, leucine zipper, and helix-turn-helix.

41. The method of claim 1, 37, or 38 in which the functional domain of interest is an SH3 domain.

42. A method of identifying a polypeptide comprising an SH3 domain of interest comprising:

(a) contacting a multivalent recognition unit complex, which complex comprises (i) avidin or streptavidin, and (ii) biotinylated recognition units, with a plurality of polypeptides from a cDNA expression library, in which the recognition unit is a peptide having in the range of 6 to 60 amino acid residues and which selectively binds an SH3 domain; and

(b) identifying a polypeptide having a selective binding affinity for said recognition unit complex.

43. The method of claim 1 in which the functional domain of interest comprises a catalytic site.

44. The method of claim 43 in which said catalytic site corresponds to that found in glutathione S-transferase.

45. A method of identifying a polypeptide comprising a functional domain of interest or a functional equivalent thereof comprising:

(a) screening a random peptide library to identify a peptide that selectively binds a functional domain of interest; and

(b) screening a cDNA or genomic expression library with said peptide or a binding portion thereof to identify a polypeptide that selectively binds said peptide.

46. The method of claim 45 in which the screening step (b) is carried out by use of said peptide in a multivalent peptide complex.

47. The method of claim 46 in which the screening step (b) is carried out by use of said peptide in a complex comprising streptavidin and biotinylated peptide.

48. The method of claim 46 in which the screening step (b) is carried out by use of said peptide in the form of multiple antigen peptides (MAP).

49. The method of claim 46 in which the screening step (b) is carried out by use of said peptide cross-linked to bovine serum albumin or keyhole limpet hemocyanin.

50. A method of identifying a polypeptide comprising a functional domain of interest or a functional equivalent thereof comprising:

(a) screening a random peptide library to identify a plurality of peptides that selectively bind a functional domain of interest;

(b) determining at least part of the amino acid sequences of said peptides;

(c) determining a consensus sequence based upon the determined amino acid sequences of said peptides; and

(d) screening a cDNA or genomic expression library with a peptide comprising the consensus sequence to identify a polypeptide that selectively binds said peptide.

51. The method of claim 50 in which the screening step (d) is carried out by use of said peptide in a multivalent peptide complex.

52. A method of identifying a polypeptide comprising a functional domain of interest or a functional equivalent thereof comprising:

(a) screening a random peptide library to identify a first peptide that selectively binds a functional domain of interest;

(b) determining at least part of the amino acid sequence of said first peptide;

(c) searching a database containing the amino acid sequences of a plurality of expressed natural proteins to identify a protein containing an amino acid sequence homologous to the amino acid sequence of said first peptide; and

(d) screening a cDNA or genomic expression library with a second peptide comprising the sequence of said protein that is homologous to the amino acid sequence of said first peptide.

53. An assay kit comprising in one or more containers:

(a) a purified polypeptide containing a functional domain of interest, in which the functional domain of is a domain selected from the group consisting of an SH1, SH2, SH3, PH, PTB, LIM, armadillo, Notch/ankyrin repeat, zinc finger, leucine zipper, and helix-turn-helix; and

(b) a purified recognition unit having a selective binding affinity for said functional domain in said polypeptide.

54. The assay kit of claim 53 in which said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 8, 10, 12, 18, 20, 22, 24, 30, 32, 38, 40, 190, 192, 194, 196, 198, 200, and 221.

55. The assay kit of claim 53 in which said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs:113-115, 118-121, 125-128, 133-139, 204-218, and 219.

56. The assay kit of claim 53 in which said recognition unit is a peptide.

57. The assay kit of claim 53 in which said polypeptide or recognition unit is labeled.

58. The assay kit of claim 57 in which said polypeptide or recognition unit is labeled with an enzyme.

59. The assay kit of claim 57 in which said polypeptide or recognition unit is labeled with an epitope.

60. The assay kit of claim 57 in which said polypeptide or recognition unit is labeled with a chromogen.

61. The assay kit of claim 57 in which said polypeptide or recognition unit is labeled with biotin.

62. The assay kit of claim 53 in which said polypeptide or recognition unit is immobilized on a solid support.

63. An assay kit comprising in containers:

(a) a plurality of purified polypeptides, each polypeptide in a separate container and each polypeptide containing a functional domain of interest in which the functional domain of interest is a domain selected from the group consisting of an SH1, SH2, SH3, PH, PTB, LIM, armadillo, Notch/ankyrin repeat, zinc finger, leucine zipper, and helix-turn-helix; and

(b) at least one recognition unit having a selective binding affinity for said functional domain in each of said plurality of polypeptides.

64. An assay kit comprising in one or more containers:

(a) a plurality of purified polypeptides, each polypeptide in a separate container and each polypeptide containing an SH3 domain; and

(b) at least one peptide having a selective affinity for the SH3 domain in each of said plurality of polypeptides.

65. A kit comprising a plurality of purified polypeptides comprising a functional domain of interest, each polypeptide in a separate container, and each polypeptide having a functional domain of a different sequence but capable of displaying the same binding specificity.

66. The kit of claim 65 in which the polypeptides have an amino acid sequence selected from the group consisting of: SEQ ID NO: 8, 10, 12, 18, 20, 22, 24, 30, 32, 38, 40, 190, 192, 194, 196, 198, 200, and 221.

67. The kit of claim 65 in which the functional domain is an SH3 domain.

68. The kit of claim 65 in which the functional domain is an SH3 domain from a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 8, 10, 12, 18, 20, 22, 24, 30, 32, 38, 40, 190, 192, 194, 196, 198, 200, and 221.

69. A method for screening a potential drug candidate comprising:

(a) allowing at least one polypeptide comprising a functional domain of interest to come into contact with at least one recognition unit having a selective affinity for said functional domain in said polypeptide, in the presence of an amount of a potential drug candidate, such that said polypeptide and said recognition unit are capable of interacting when brought into contact with one another in the

absence of said drug candidate, and in which the functional domain of interest is a domain selected from the group consisting of an SH1, SH2, SH3, PH, PTB, LIM, armadillo, Notch/ankyrin repeat, zinc finger, leucine zipper, and helix-turn-helix; and

(b) determining the effect, if any, of the presence of the amount of said drug candidate on the interaction of said polypeptide with said recognition unit.

70. The method of claim 69 in which the effect of the drug candidate upon multiple, different interacting polypeptide-recognition unit pairs is determined in which at least some of said polypeptides have a functional domain that differs in sequence but is capable of displaying the same binding specificity as the functional domain in another of said polypeptides.

71. The method of claim 69 in which at least one of said at least one polypeptide or recognition unit contains a consensus functional domain and consensus recognition unit, respectively.

72. The method of claim 69 in which the polypeptide is a polypeptide identified by the method of claim 1.

73. The method of claim 69 in which the drug candidate is an inhibitor of the polypeptide-recognition unit interaction that is identified by detecting a decrease in the binding of polypeptide to recognition unit in the presence of such inhibitor.

74. A purified polypeptide comprising an SH3 domain, said SH3 domain having an amino acid sequence selected from the group consisting of: SEQ ID NOs:113-115, 118-121, 125-128, 133-139, 204-218, and 219.

75. A purified polypeptide comprising an SH3 domain, said polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOs: 8, 10, 12, 18, 20, 22, 24, 30, 32, 38, 40, 190, 192, 194, 196, 198, 200, and 221.

76. A purified DNA encoding an SH3 domain, said DNA having a sequence selected from the group consisting of SEQ ID NOs: 7, 9, 11, 17, 19, 21, 23, 29, 31, 37, 39, 189, 191, 193, 195, 197, 199, and 220.

77. A purified DNA encoding a polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NOs: 8, 10, 12, 18, 20, 22, 24, 30, 32, 38, 40, 190, 192, 194, 196, 198, 200, and 221.

78. A purified DNA encoding a polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NOs:113-115, 118-121, 125-128, 133-139, 204-218, and 219.

79. A purified molecule comprising an SH3 domain of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 8, 10, 12, 18, 20, 22, 24, 30, 32, 38, 40, 190, 192, 194, 196, 198, 200, and 221.

80. A fusion protein comprising (a) an amino acid sequence comprising an SH3 domain of a polypeptide having the amino acid sequence of SEQ ID NO: 8, 10, 12, 18, 20, 22, 24, 30, 32, 38, 40, 190, 192, 194, 196, 198, 200, or 221 joined via a peptide bond to (b) an amino acid sequence of at least six amino acids from a different polypeptide.

81. A purified DNA encoding the fusion protein of claim 80.

82. A nucleic acid vector comprising the DNA of claim 81.

83. A nucleic acid vector comprising the DNA of claim 76.

84. A nucleic acid vector comprising the DNA of claim 78.

85. A recombinant cell containing the nucleic acid vector of claim 82, 83, or 84.

86. A purified nucleic acid hybridizable to a nucleic acid having a sequence selected from the group consisting of: SEQ ID NOs: 7, 9, 11, 17, 19, 21, 23, 29, 31, 37, 39, 189, 191, 193, 195, 197, 199, and 220.

87. A method of producing the fusion protein of claim 80 comprising culturing a recombinant cell containing a nucleic acid vector encoding said fusion protein such that said fusion protein is expressed, and recovering the expressed fusion protein.

88. A method of producing the polypeptide of claim 74 comprising culturing a recombinant cell containing a nucleic acid vector encoding said polypeptide such that said polypeptide is expressed, and recovering the expressed polypeptide.

89. The method of claim 69 in which said polypeptide is a polypeptide containing an SH3 domain produced by a method comprising:

(i) screening a peptide library with an SH3 domain to obtain one or more peptides that bind the SH3 domain;

(ii) using one of the peptides from step (i) to screen a source of polypeptides to identify one or more polypeptides containing an SH3 domain;

(iii) determining the amino acid sequence of the polypeptides identified in step (ii); and

(iv) producing the one or more novel polypeptides containing an SH3 domain.

90. The method of claim 69 in which said polypeptide is a polypeptide containing an SH3 domain produced by a method comprising:

(i) screening a peptide library with an SH3 domain to obtain a plurality of peptides that bind the SH3 domain;

(ii) determining a consensus sequence for the peptides obtained in step (i);

(iii) producing a peptide comprising the consensus sequence;

(iv) using the peptide comprising the consensus sequence to screen a source of polypeptides to identify one or more polypeptides containing an SH3 domain;

(v) determining the amino acid sequence of the polypeptides identified in step (iv); and

(vi) producing the one or more polypeptides containing an SH3 domain.

91. A method of determining the potential pharmacological activities of a molecule comprising:

(a) contacting the molecule with a compound comprising a functional domain under conditions conducive to binding;

(b) detecting or measuring any specific binding that occurs; and

(c) repeating steps (a) and (b) with a plurality of different compounds, each compound comprising a functional domain of different sequence but capable of displaying the same binding specificity.

92. The method of claim 91 in which the functional domain is an SH3 domain.

93. The method of claim 92 in which the compounds comprise the SH3 domains of Src, Abl, Cortactin, Phospholipase

Cγ, Nck, Crk, p53bp2, Amphiphysin, Grb2, RasGap, or Phosphatidylinositol 3' kinase.

94. A method of identifying a compound that affects the binding of a molecule comprising a functional domain to a recognition unit that selectively binds to the functional domain comprising:

(a) contacting the molecule comprising the functional domain and the recognition unit under conditions conducive to binding in the presence of a candidate compound and measuring the amount of binding between the molecule and the recognition unit and in which the functional domain of interest is a domain selected from the group consisting of an SH1, SH2, SH3, PH, PTB, LIM, armadillo, Notch/ankyrin repeat, zinc finger, leucine zipper, and helix-turn-helix;

(b) comparing the amount of binding in step (a) with the amount of binding known or determined to occur between the molecule and the recognition unit in the absence of the candidate compound, where a difference in the amount of binding between step (a) and the amount of binding known or determined to occur between the molecule and the recognition unit in the absence of the candidate compound indicates that the candidate compound is a compound that affects the binding of the molecule comprising a functional domain and the recognition unit.

95. The method of claim 94 in which the functional domain is an SH3 domain.

96. The method of claim 20 in which the recognition unit complex is a complex comprising (a) streptavidin conjugated to alkaline phosphatase; and (b) the biotinylated peptides.

97. A method of identifying a polypeptide comprising a functional domain of interest comprising:

(a) contacting a recognition unit that is a peptide having 140 amino acids or fewer with a plurality of polypeptides; and

(b) identifying a polypeptide having a selective binding affinity for said recognition unit complex.

98. An antibody to a polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NOs:113-115, 118-121, 125-128, 133-139, 204-218, and 219.

99. An antibody to a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 8, 10, 12, 18, 20, 22, 24, 30, 32, 38, 40, 190, 192, 194, 196, 198, 200, and 221.

100. The purified nucleic acid of claim 86 that is a human nucleic acid encoding a polypeptide containing a functional domain.

101. A purified protein encoded by a first nucleic acid comprising a human cDNA or genomic sequence hybridizable to a second nucleic acid having a sequence selected from the group consisting of: SEQ ID NOs:7, 9, 11, 17, 19, 21, 29, and 31.

102. The assay kit of claim 53 in which said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs:6, 14, 16, 26, 28, 34, 36, 112, 116, 117, 122-124, 129-132, and 140.